## Amendments to the Claims

1-16. (Cancelled)

17. (Currently amended) An apparatus for analysing a polynucleotide, the apparatus comprising an impermeable support segregated into at least two defined cells, the cells having oligonucleotides containing predetermined sequences covalently attached thereto, wherein the sequence of the oligonucleotides of a first cell is different from the sequence of the oligonucleotides of a second cell, and wherein a terminal nucleotide of each oligonucleotide is covalently attached to the surface of the support ~~each oligonucleotide is bound to the support by a covalent link through a terminal nucleotide~~.

18. (Previously presented) The apparatus of claim 17, wherein the length of each oligonucleotide is from 8 to 20 nucleotides.

19. (Currently amended) The apparatus of claim 17, wherein the cells have a size of about 10~~μm~~ microns to about 100~~μm~~ microns.

20. (Previously presented) The apparatus of claim 17, wherein the cells are separated by a solvent-repellent grid.

21. (Previously presented) The apparatus of claim 17, wherein the impermeable support is glass.

22. (Cancelled)

23. (Previously presented) The apparatus of claim 17, comprising between 72 and $1.1 \times 10^{12}$ cells.

24. (Previously presented) The apparatus of claim 17, comprising $4^S$ oligonucleotide sequences of length $s$, wherein $s \geq 4$, and comprises $4^S$ cells.

25. (Previously presented) The apparatus of claim 17, wherein the oligonucleotides in the cells have overlapping sequences for mismatch scanning of the polynucleotide.

26. (Currently amended) An apparatus for analysing a polynucleotide, the apparatus comprising an impermeable glass plate with patches of microporous glass, the patches defining cells of an array, each cell having oligonucleotides containing predetermined sequences covalently attached thereto, wherein the sequence of the oligonucleotides of a first cell is different from the sequence of the oligonucleotides of a second cell.

27. (Previously presented) The apparatus of claim 26, wherein the length of each oligonucleotide is from 8 to 20 nucleotides.

28. (Currently amended) The apparatus of claim 26, wherein the cells have a size of about 10~~μm~~ microns to about 100~~μm~~ microns.

29. (Currently amended) The apparatus of claim 26, wherein a terminal nucleotide of each oligonucleotide is covalently attached to a patch of the support ~~each oligonucleotide is bound to a patch by a covalent link through a terminal nucleotide~~.

30. (Previously presented) The apparatus of claim 26, comprising between 72 and $1.1 \times 10^{12}$ cells.

31. (Previously presented) The apparatus of claim 26, comprising $4^S$ oligonucleotide sequences of length *s*, wherein $s \geq 4$, and comprises $4^S$ cells.

32. (Previously presented) The apparatus of claim 26, wherein the oligonucleotides in the cells have overlapping sequences for mismatch scanning of the polynucleotide.

33. (Previously presented) A method for analysing a polynucleotide, comprising the steps of:

labelling the polynucleotide or fragments of the polynucleotide, to produce labelled nucleic acid;

applying the labelled nucleic acid under hybridisation conditions to the array of claim 17, and

observing the cells in the array to which the labelled nucleic acid hybridises.

34. (Previously presented) The method of claim 33, wherein the polynucleotide is randomly degraded to form a mixture of oligonucleotides of chosen lengths, the mixture being thereafter labelled to form labelled nucleic acid which is applied to the array.

35. (Currently amended) The method of claim 33, wherein the polynucleotide or fragments of the polynucleotide are labelled with $^{32}P$ ~~or a fluorescent label~~.

36. (Currently amended) The method of claim 33, wherein the polynucleotide or fragment of the polynucleotide are populations of mRNA ~~or genomic DNA~~.

37. (Previously presented) A method for analysing a polynucleotide, comprising the steps of:

labelling the polynucleotide or fragments of the polynucleotide, to produce labelled nucleic acid;

applying the labelled nucleic acid under hybridisation conditions to the array of claim 26; and

observing the cells in the array to which the labelled nucleic acid hybridises.

38. (Previously presented) The method of claim 37, wherein the polynucleotide is randomly degraded to form a mixture of oligonucleotides of chosen lengths, the mixture being thereafter labelled to form labelled nucleic acid which is applied to the array.

39. (Currently amended) The method of claim 37, wherein the polynucleotide or fragments of the polynucleotide are labelled with $^{32}P$ ~~or a fluorescent label~~.

40. (Currently amended) The method of claim 37, wherein the polynucleotide or fragment of the polynucleotide are populations of mRNA ~~or genomic DNA~~.

41. (New) The method of claim 33, wherein the polynucleotide or fragments of the polynucleotide are labelled with a fluorescent label.

42. (New) The method of claim 33, wherein the polynucleotide or fragment of the polynucleotide are populations of genomic DNA.

43. (New) The method of claim 37, wherein the polynucleotide or fragments of the polynucleotide are labelled with a fluorescent label.

44. (New) The method of claim 37, wherein the polynucleotide or fragment of the polynucleotide are populations of genomic DNA.